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Figure 1A

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| | | |
|-----|---|-----|
| 1 | ATGAGCTCCGCATGCCAGGGCGCTGCCCTAGTCGTACCCCTCTCCACTTGACCAGG | 60 |
| 1 | M S S R I A R A L A L V V T L L H L T R | 20 |
| 61 | CTGGCGCTCTCACCGCCCTGCCACTGCCCTGGAGGCGCCAAGTGCAGCG | 120 |
| 21 | L A L S T C P A A C H C P L E A P K C A | 40 |
| 121 | CCGGGAGTCGGGCTGGTCCGGGACGGCTGGCCTGCTGTAAGGTCTGCGCCAAGCAGCTC | 180 |
| 41 | P G V G L V R D G C G C C K V C A K Q L | 60 |
| 181 | AACGAGGACTGCAGAAAAGCAGCCCTGCGACCACACCAAGGGCTGGAATGCAACTTC | 240 |
| 61 | N E D C S K T Q P C D H T K G L E C N F | 80 |
| 241 | GGCGCCAGCTCACCGCTCTGAAGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCCTGT | 300 |
| 81 | G A S S T A L K G I C R A Q S E G R P C | 100 |
| 301 | GAATATAACTCCAGAACTACCAAAAGGGAAAGTTCCAGCCCCACTGTAAACATCAG | 360 |
| 101 | E Y N S R I Y Q N G E S F Q P N C K H Q | 120 |
| 361 | TGCACATGTATTGATGGCGCCGTGGCTGCATTCCCTCTGTGTCCCCAAGAACTATCTCTC | 420 |
| 121 | C T C I D G A V G C I P L C P Q E L S L | 140 |
| 421 | CCCAACTTGGGCTGTCCCAACCCCTGGCTGGTCAAAGTTACCCGGCAGTGCAGGGAG | 480 |
| 141 | P N L G C P N P R L V K V T G Q C C E E | 160 |
| 481 | TGGGTCTGTGACGAGGATAGTATCAAGGACCCATGGAGGACCAGGACGGCCTCCTGGC | 540 |
| 161 | W V C D E D S I K D P M E D Q D G L L G | 180 |
| 541 | AAGGAGCTGGGATTCGATGCCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA | 600 |
| 181 | K E L G F D A S E V E L T R N N E L I A | 200 |
| 601 | GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTGGAAATGGAGCTCGCATCCTA | 660 |
| 201 | V G K G S S L K R L P V F G M E P R I L | 220 |
| 661 | TACAACCCTTACAAGGCCAGAAATGTTAACAAACTTCATGGTCCCAGTGCCTCA | 720 |
| 221 | Y N P L Q G Q K C I V Q T T S W S Q C S | 240 |
| 721 | AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCCTGAGTGCCGCC | 780 |
| 241 | K T C G T G I S T R V T N D N P E C R L | 260 |
| 781 | GTGAAAGAAACCCGGATTGTGAGGTGCGGCCCTGTGGACAGCCAGTGTACAGCAGCCTG | 840 |
| 261 | V K E T R I C E V R P C G Q P V Y S S L | 280 |

Sanger Institute
Genomic DNA Sequencing

Figure 1B
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| | | |
|------|--|------|
| 841 | AAAAAGGGCAAGAAAATGCAGCAAGACCAAGAAAATCCCCCGAACCCAGTCAGGTTACTTAC | 900 |
| 281 | K K G K K C S K T K K S P E P V R F T Y | 300 |
| 901 | GCTGGATGTTGACTGTGAAGAAAATACCGGCCAAGTACTGCGGTTCTGCGTGGACGGC | 960 |
| 301 | A G C L S V K K Y R P K Y C G S C V D G | 320 |
| 961 | CGATGCTGCACGCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG | 1020 |
| 321 | R C C T P Q L T R T V K M R F R C E D G | 340 |
| 1021 | GAGACATTTCCAAGAACGTCAATGATGATCCAGTCCTGCAAATGCAACTACAACGCCG | 1080 |
| 341 | E T F S K N V M M I Q S C K C N Y N C P | 360 |
| 1081 | CATGCCAATGAAGCAGCGTTCCCTTCTACAGGCTGTTCAATGACATTACAAATTAGG | 1140 |
| 361 | H A N E A A F P F Y R L F N D I H K F R | 380 |
| 1141 | GAATTA 1146 | |
| 381 | D * 382 | |

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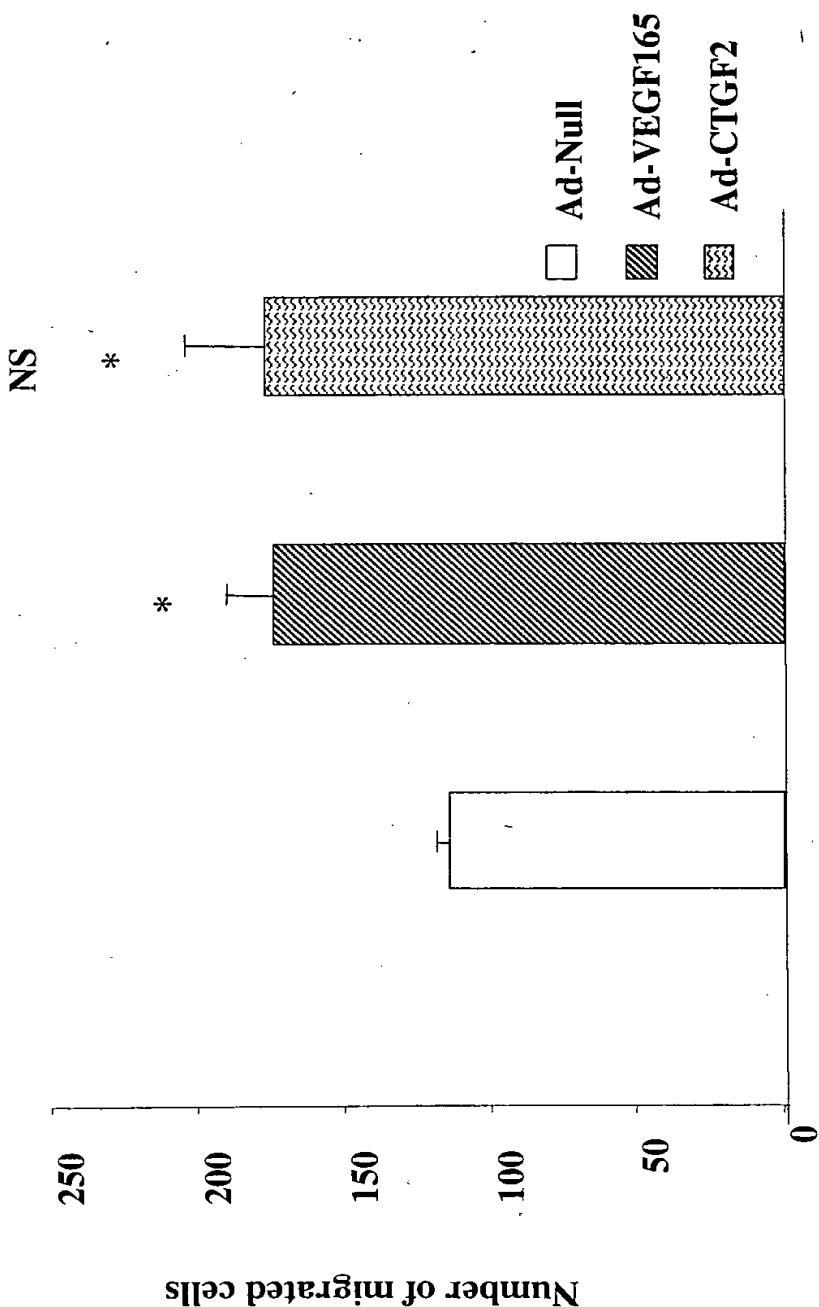


Figure 2

Figure 3

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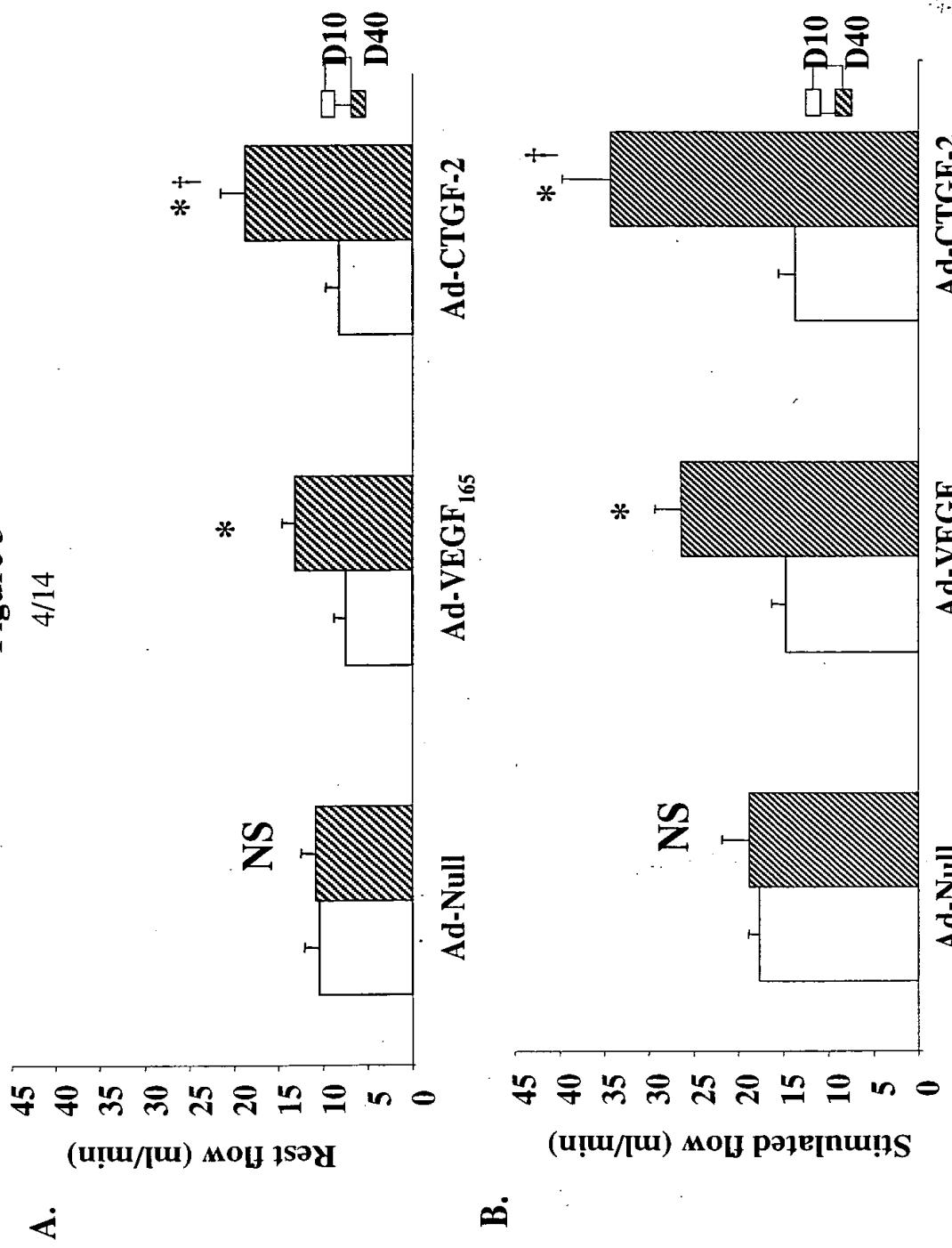


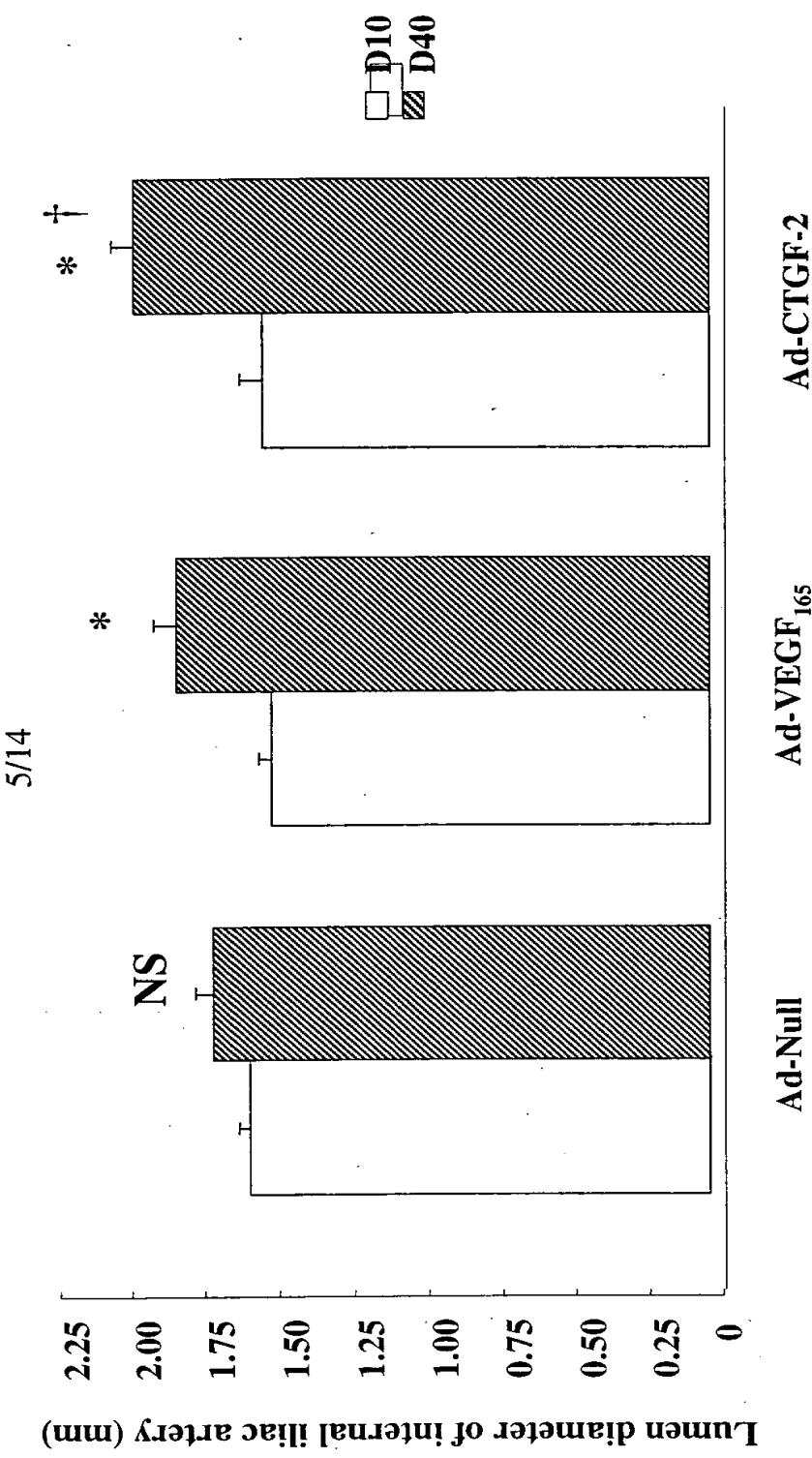
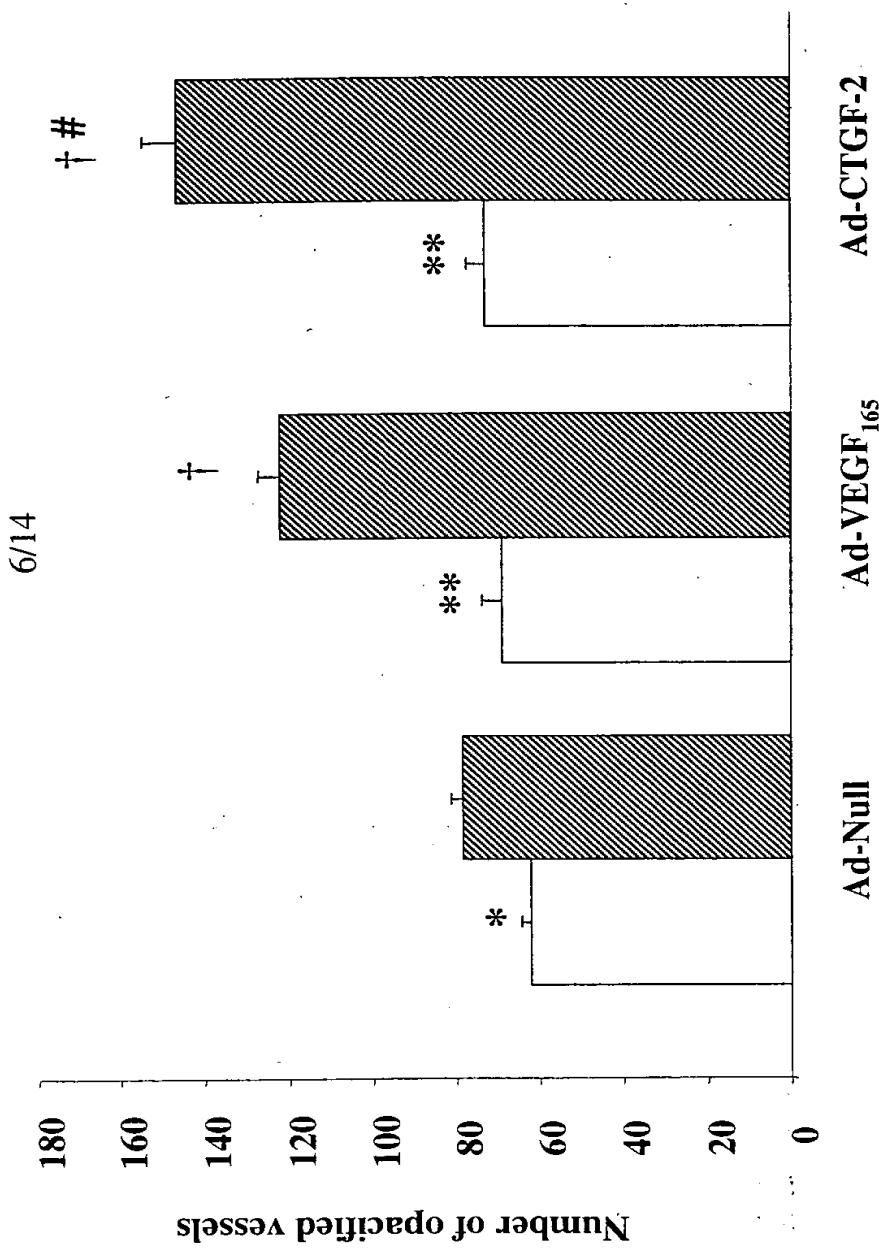
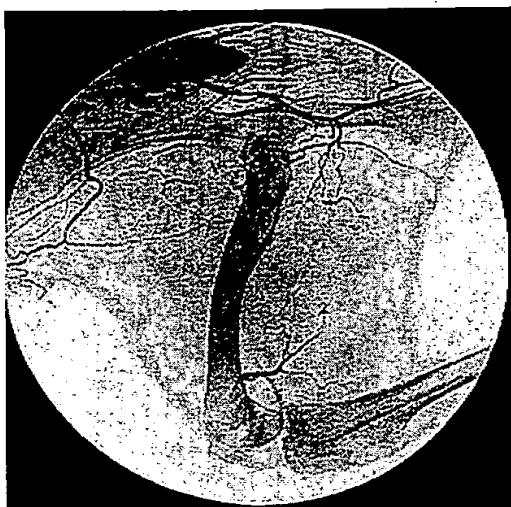
Figure 4

Figure 5

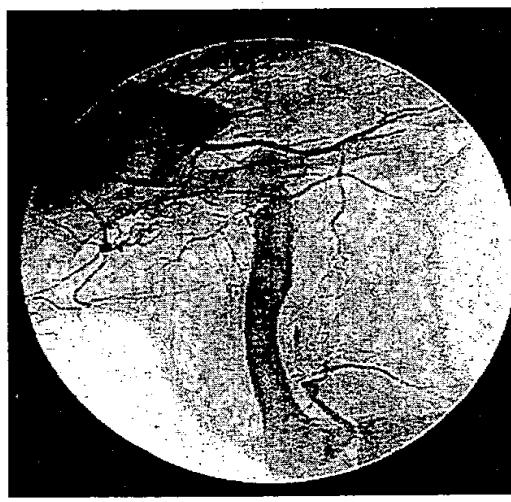
Tumor angiogenesis
inhibition by
Ad-VEGF-165
and Ad-CTGF-2

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Ad-CTGF2



Ad-VEGFR165



Ad-Null

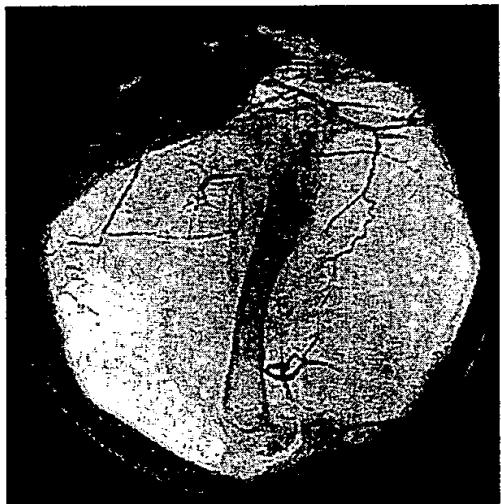
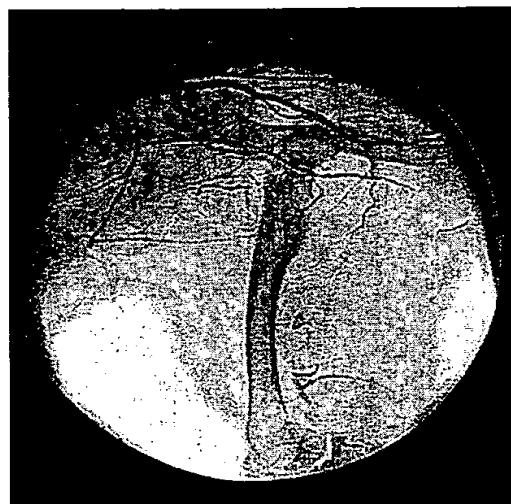
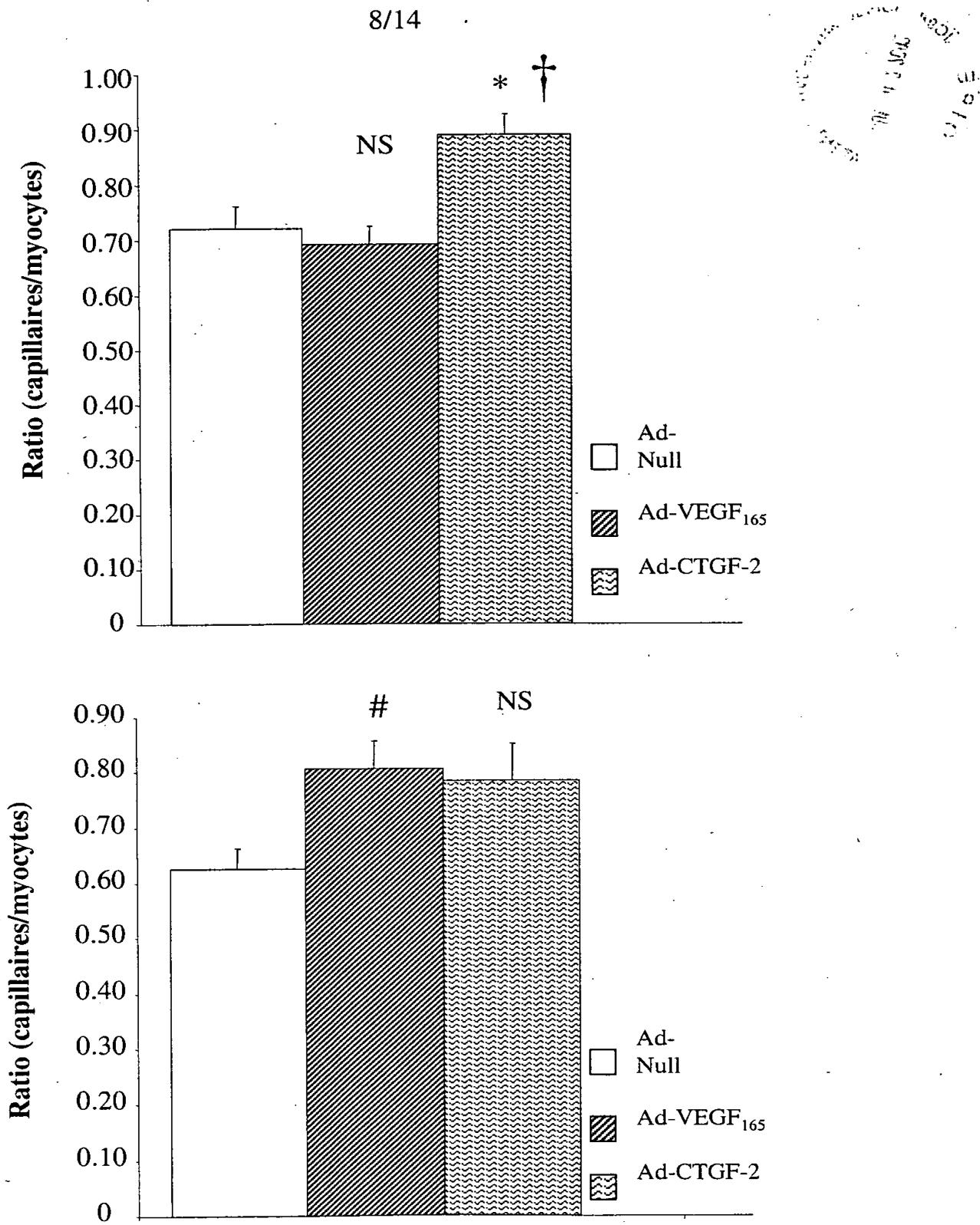
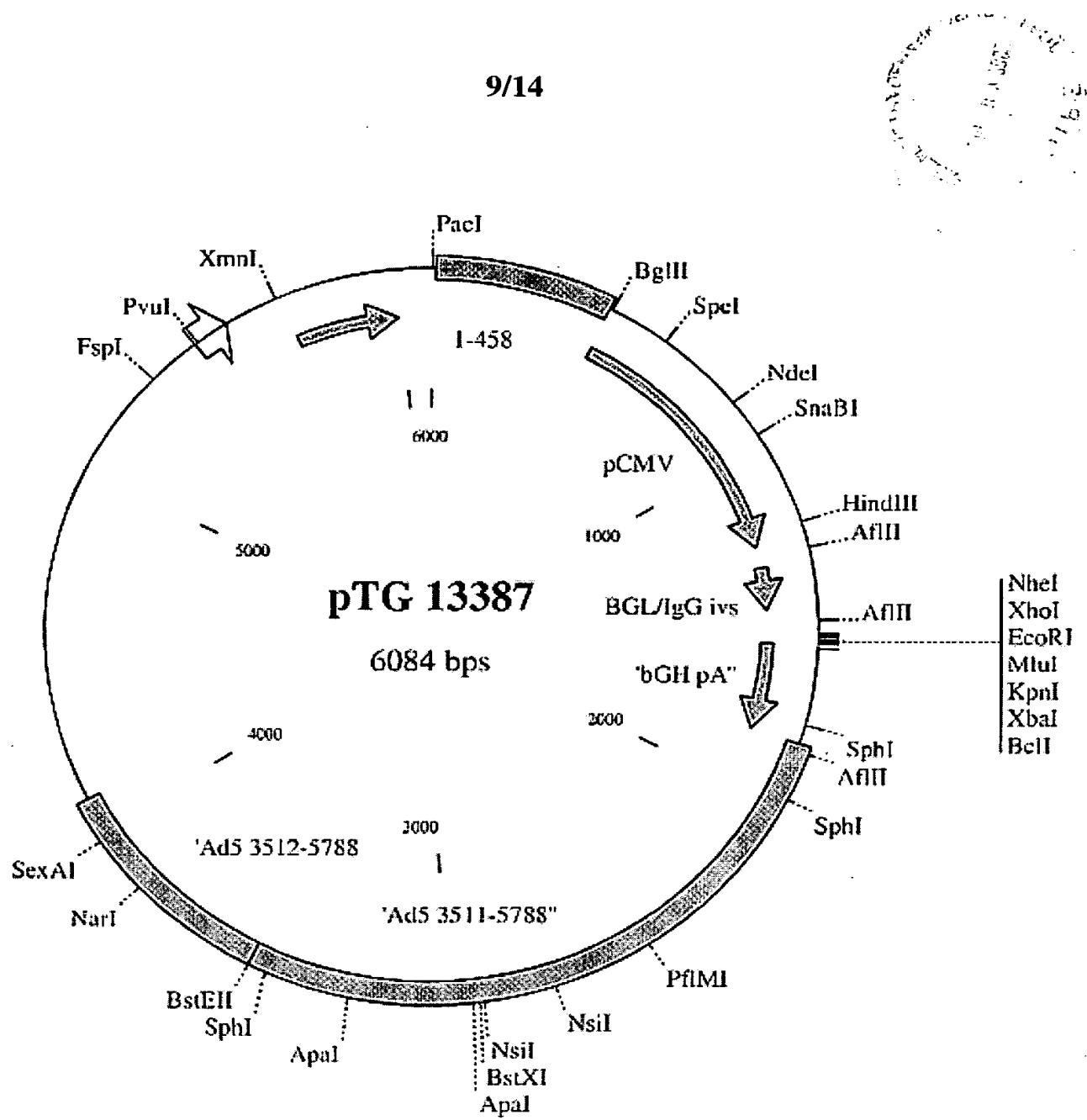


Figure 6

**Figure 7**

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**Figure 8**

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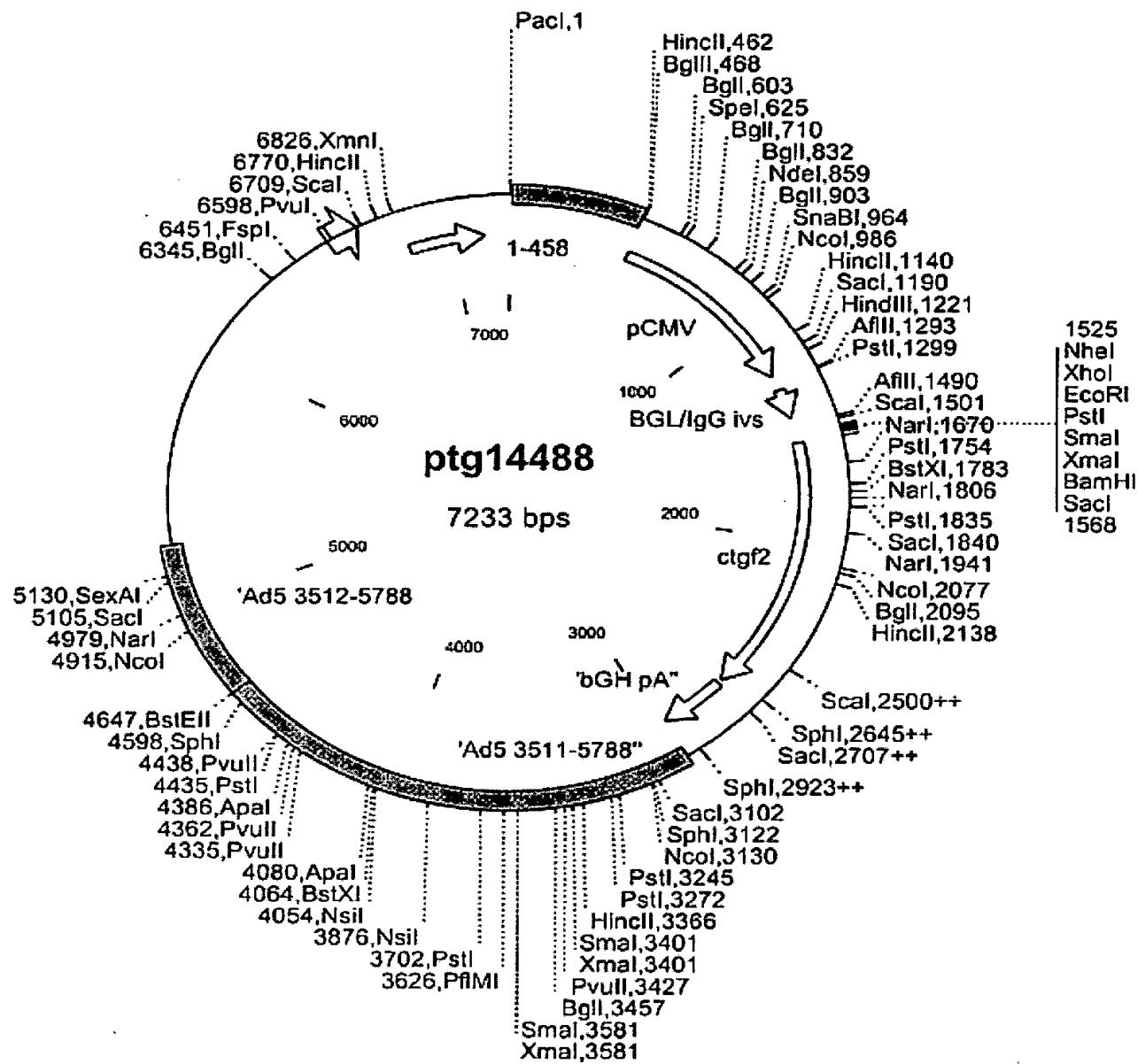
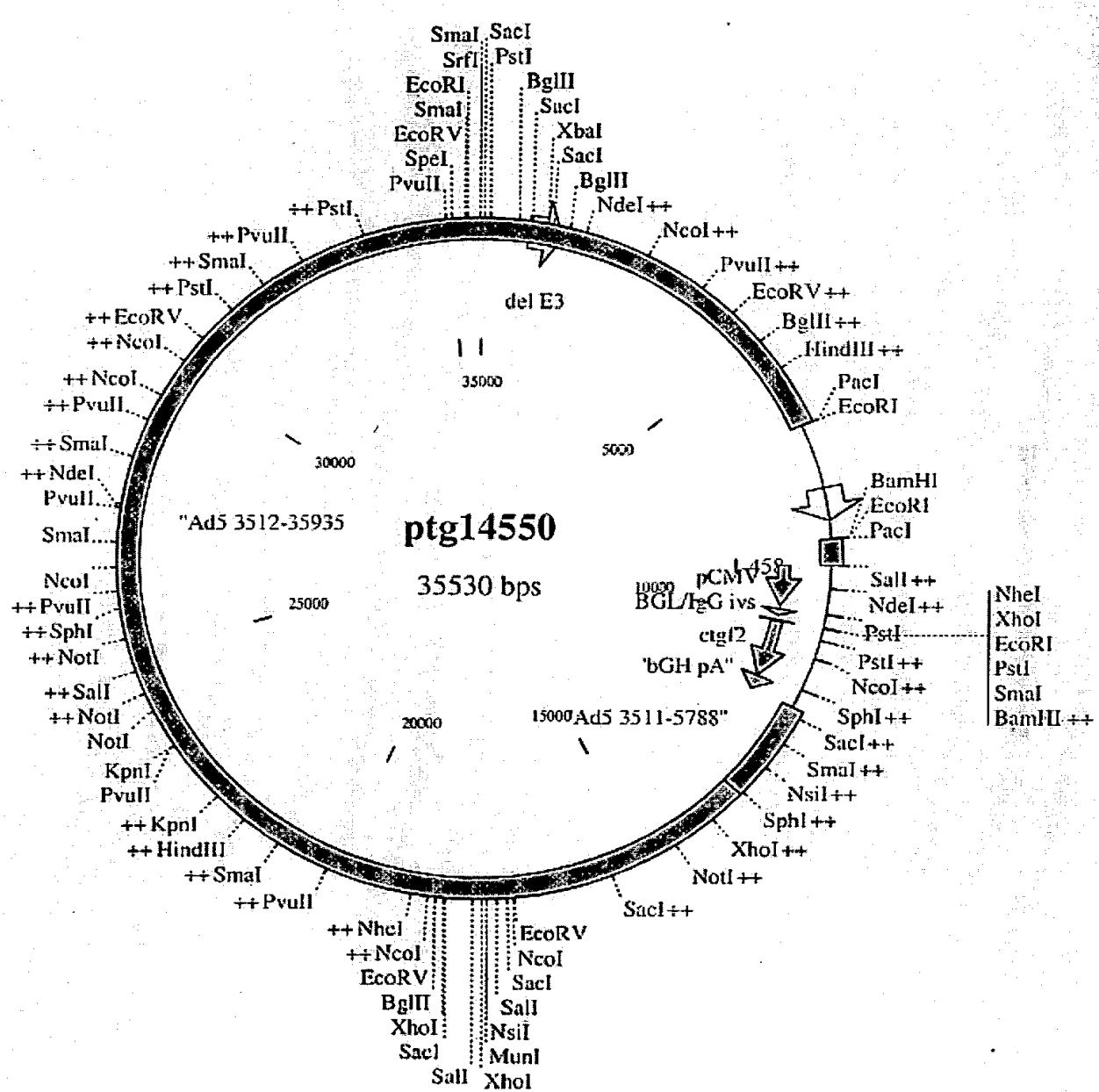


Figure 9

Figure 10
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09901910 . 070202

Figure 11A
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ATGAGCTCCCGAATCGTCAGGGAGCTGCCCTTAGTCGTACCCCTTCTCCACTTGACCAAGG
M S S R I V R E L A L V V T L L H L T R

GTGGGCTCTCACCTGCCCGCTGAAGTGCCTACTGCCACTGGCCCCCTGGAGGCCAACAGTGCAGC
V G L S T C P A D C H C P L E A P K C A

CGGGAGCTGGCTGGTCCGGGACGGCTGGCTGGTGTAAAGGTCTGCCCAAGCAGCTC
P G V G L V R D G C G C C K V C A K Q L

AACGAGGACTGCAGAAAAACGGCCCTCTGCAGAGCACACCAAGGGCTGGAAATGCCAAACTTC
N E D C R K T Q P C D H T K G L E C N F

GGGCCAGCTCACCGCTCTGAAGGGATCTGCAGAGCTCAGTCAGGGAGACCCCTGT
G A S S T A L K G I C R A Q S E G R P C

GAATAACTCAGAATCTACCAAAACGGGAAAGTTCCAGCCAACTGTAACATCAG
E Y N S R I Y Q N G E S F Q P N C K H Q

TGGCATGTATGGATGGGGGGGGCTTGCATTCCCTCTGTGTCCCCAAGAACTATCT
C T C I G W R R G A C I P L C P Q E L S

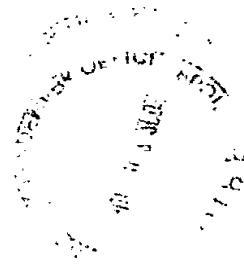


Figure 11B
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C⁺TCCCCAACTGGCTGCCAACCCCTGGCTGGTCAAAGT⁺TACCGGGCA⁺GTCGCGAG
 L P N L G C P N P R L V K V T G Q C C E
 GAGTGGGTCTGTGACGAGGATA⁺TATCAAGGACC⁺CCATGGGAC⁺GGACGGCCTCCTT
 E W V C D E D S I K D P M E D Q D G L L
 GGCAAGGGCTGGGATTGGATCGGATGCCCTCCGAGGTGGACTTGACCAAGAAA⁺CATGAATTGATT
 G K G L G F D A S E V E L T R N N E L I
 GCAGTTGGAAAAGGCAGGCTCACTGAAGGGC⁺GGCTCCCTGTTGGAA⁺ATGGAGCCTCGC⁺ATC
 A V G K G S S L K R L P V F G M E P R I
 CTATACAACCCTTACAAGGCCAGAA⁺ATGTATTGTTCAAACAA⁺ACTTCATGGTCCCAGTG
 L Y N P L Q G Q K C I V Q T T S W S Q C
 TCAAAGACCTGTTGAA⁺ACTGGTATCTCCACACGAGTTACCAAA⁺TGACAACCCTGAGTGGCGC
 S K T C G T G I S T R V T N D N P E C R
 CTTGGAAAAGAAACCCGGATTGGAGGTGGCTTGAGGACAGGCCAGGTACAGCAGC
 L V K E T R I C E V R P C G Q P V Y S S

0 9 9 0 1 9 1 0 , 0 7 0 2 0 2

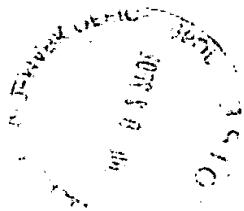


Figure 11C
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CTGAAAAGGGCAAGAAATGCCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTACT
L K G K C S K T K S P E P V R F T

TACGCTGGATGTTGAGTGTGAAGAAATAACGGGCCAACGTAATGCCGTTCCCTGCCGTGGAC
Y A G C L S V K K Y R P K Y C G S C V D

GGCGATGCTGCACGCCCAAGCTGACCAAGACTGTGAAGATGCCGTTCCCTGCCGAAGAT
G R C C T P Q L T R T V K M R F P C E D

GGGAGACATTCCAAGAACGTCATGATGATCCAGTCCTCAAATGCAACTACAATGCG
G E T F S K N V M M I Q S S K C N Y N C

CCGCAATGCCAATGAAAGCAGCGTTCCCTCTACAGGCTGTTCAAATGAA
P H A N E A A F P F V R L F Q